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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=4; day=29; hr=15; min=13; sec=2; ms=758;]

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Application No: 10564458 Version No: 2.0

Input Set:

Output Set:

Started: 2008-04-15 15:58:26.350
Finished: 2008-04-15 15:58:31.867
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 517 ms
Total Warnings: 109
Total Errors: 0
No. of SeqIDs Defined: 109
Actual SeqID Count: 109

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-04-15 15:58:26.350
Finished: 2008-04-15 15:58:31.867
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 517 ms
Total Warnings: 109
Total Errors: 0
No. of SeqIDs Defined: 109
Actual SeqID Count: 109

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21) This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (44)
W 402	Undefined organism found in <213> in SEQ ID (106)
W 402	Undefined organism found in <213> in SEQ ID (107)

SEQUENCE LISTING

<110> Anderson, Annaliesa S.
Jansen, Kathrin Ute
Kelly, Rosemarie
Schultz, Loren D.
Montgomery, Donna L.
McClements, William L.

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE
IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

<130> 21569YP

<140> 10564458
<141> 2006-01-12

<150> PCT/2004/023523

<151> 2004-07-22

<150> 60/489,840
<151> 2003-07-24

<150> 60/520,115
<151> 2003-11-14

<160> 109

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 446
<212> PRT
<213> Artificial Sequence

<220>

<223> ORF0657nI with amino terminus methionine

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1 5 10 15
Glu Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr
20 25 30
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala
35 40 45
Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala
50 55 60
Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn
65 70 75 80
Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro
85 90 95
Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp
100 105 110
Phe Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala

115	120	125
Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu		
130	135	140
Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val		
145	150	155
Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr		160
165	170	175
Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys		
180	185	190
Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys		
195	200	205
Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala		
210	215	220
Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala		
225	230	235
Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn		240
245	250	255
Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys		
260	265	270
Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala		
275	280	285
Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp		
290	295	300
Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu		
305	310	315
Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu		320
325	330	335
Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp		
340	345	350
Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp		
355	360	365
Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys		
370	375	380
Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr		
385	390	395
Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys		400
405	410	415
Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala		
420	425	430
Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro		
435	440	445

<210> 2

<211> 645

<212> PRT

<213> S. aureus

<400> 2

Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys		
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Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu		
20	25	30
Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr		
35	40	45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr		
50	55	60

Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65 70 75 80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
85 90 95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
100 105 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
115 120 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
130 135 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145 150 155 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
165 170 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
180 185 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
195 200 205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
210 215 220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225 230 235 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
245 250 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
260 265 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
275 280 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
290 295 300
Lys Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp Thr Lys Lys Ala
305 310 315 320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
325 330 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
340 345 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
355 360 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
370 375 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385 390 395 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
405 410 415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
420 425 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
435 440 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
450 455 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465 470 475 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
485 490 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
500 505 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys

515	520	525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val		
530	535	540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys		
545	550	555
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys		560
565	570	575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly		
580	585	590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys		
595	600	605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro		
610	615	620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro		
625	630	635
Arg Lys Arg Lys Asn		640
	645	

<210> 3
<211> 569
<212> PRT
<213> Artificial Sequence

<220>
<223> ORF0657nH with amino terminus methionine

<400> 3		
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15		
Glu Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr		
20	25	30
30		
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala		
35	40	45
45		
Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala		
50	55	60
60		
Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn		
65	70	75
80		
Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro		
85	90	95
95		
Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp		
100	105	110
110		
Phe Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala		
115	120	125
125		
Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu		
130	135	140
140		
Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val		
145	150	155
160		
Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr		
165	170	175
175		
Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys		
180	185	190
190		
Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys		
195	200	205
205		
Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala		
210	215	220
220		
Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala		

225	230	235	240												
Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn
	245		250												255
Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys
	260		265												270
Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala
	275		280												285
Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp
	290		295												300
Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu
	305		310												320
Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu
	325		330												335
Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp
	340		345												350
Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp
	355		360												365
Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys
	370		375												380
Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr
	385		390												400
Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys
	405		410												415
Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala
	420		425												430
Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro
	435		440												445
Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys
	450		455												460
Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly
	465		470												480
Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser
	485		490												495
Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala
	500		505												510
Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr
	515		520												525
Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala
	530		535												540
Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys
	545		550												560
Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser							
	565														

<210> 4

<211> 570

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH with amino terminus methionine-glycine

<400> 4

Met Gly Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys

1 5 10 15

Thr Glu Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu

	20	25	30
Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu			
35	40	45	
Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys			
50	55	60	
Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn			
65	70	75	80
Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn			
85	90	95	
Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile			
100	105	110	
Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr			
115	120	125	
Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro			
130	135	140	
Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu			
145	150	155	160
Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp			
165	170	175	
Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr			
180	185	190	
Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu			
195	200	205	
Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser			
210	215	220	
Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu			
225	230	235	240
Ala Pro Tyr Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu			
245	250	255	
Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys			
260	265	270	
Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser			
275	280	285	
Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr			
290	295	300	
Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn			
305	310	315	320
Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met			
325	330	335	
Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr			
340	345	350	
Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys			
355	360	365	
Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly			
370	375	380	
Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp			
385	390	395	400
Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr			